RAW SEQUENCE LISTING

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Application Serial Number: _10/538,922_

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PATENT APPLICATION: US/10/538,922   TIME: 13:35:18

Input Set : A:\10-538,922 Sequence Listing.TXT
Output Set: N:\CRF4\08142006\J538922.raw

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 3 <110> APPLICANT: CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
 5 <120> TITLE OF INVENTION: METHOD OF DIAGNOSIS OF OBESITY
 7 <130> FILE REFERENCE: Q88618
 9 <140> CURRENT APPLICATION NUMBER: US 10/538,922
10 <141> CURRENT FILING DATE: 2005-06-13
12 <150> PRIOR APPLICATION NUMBER: EP 02 293 085
13 <151> PRIOR FILING DATE: 2002-12-13
15 <160> NUMBER OF SEQ ID NOS: 15
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1758
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <223> OTHER INFORMATION: gad2 gene
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29 gagaatcccg gcacagcgcg agcctggtgc caagtggctc agaagttcac gggcggcatc 120
30 ggaaacaaac tgtgcgccct gctctacgga gacgccgaga agccggcgga gagcggcggg 180
31 agccaacccc cgcgggccgc cgcccggaag gccgcctgcg cctgcgacca gaagccctgc 240
32 agctgctcca agtggatgt caactacgcg tttctccatg caacagacct gctgccggcg 300
33 tgtgatggag aaaggcccac tttggcgttt ctgcaagatg ttatgaacat tttacttcag 360
34 tatgtggtga aaagtttcga tagatcaacc aaagtgattg atttccatta tcctaatgag 420
35 cttctccaag aatataattg ggaattggca gaccaaccac aaaatttgga ggaaattttg 480
36 atgcattgcc aaacaactct aaaatatgca attaaaacag ggcatcctag atacttcaat 540
37 caacttttcta ctggtttgga tatggttgga ttagcagcag actggctgac atcaacagca 600
38 aatactaaca tgttcaccta tgaaattgct ccagtatttg tgcttttgga atatgtcaca 660
39 ctaaagaaaa tgagagaaat cattggctgg ccagggggct ctggcgatgg gatattttct 720
40 cccggtggcg ccatatctaa catgtatgcc atgatgatcg cacgctttaa gatgttccca 780
41 gaagtcaagg agaaaggaat ggctgctctt cccaggctca ttgccttcac gtctgaacat 840
42 agtcatttt ctctcaagaa gggagctgca gccttaggga ttggaacaga cagcgtgatt 900
43 ctgattaaat gtgatgagag agggaaaatg attccatctg atcttgaaag aaggattctt 960
44 gaagccaaac agaaagggt tgttcctttc ctcgtgagtg ccacagctgg aaccaccgtg 1020
45 tacggagcat ttgacccct cttagctgtc gctgacattt gcaaaaagta taagatctgg 1080
46 atgcatgtgg atgcagcttg gggtggggga ttactgatgt cccgaaaaca caagtggaaa 1140
47 ctgagtggcg tggagagggc caactctgtg acgtggaatc cacacaagat gatgggagtc 1200
48 cctttgcagt gctctgctct cctggttaga gaagagggat tgatgcagaa ttgcaaccaa 1260
49 atgcatgcct cctacctctt tcagcaagat aaacattatg acctgtccta tgacactgga 1320
50 gacaaggcct tacagtgcgg acgccacgtt gatgttttta aactatggct gatgtggagg 1380
51 gcaaagggga ctaccgggtt tgaagcgcat gttgataaat gtttggagtt ggcagagtat 1440
52 ttatacaaca tcataaaaaa ccgagaagga tatgagatgg tgtttgatgg aagcctcag 1500
53 cacacaaatg tctgcttctg gtacattcct ccaagcttgc gtactctgga agacaatgaa 1560
54 gagagaatga gtcgcctctc gaaggtggct ccagtgatta aagccagaat gatggagtat 1620
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55 ggaaccacaa tggtcagcta ccaacccttg ggagacaagg tcaatttctt ccgcatggtc 1680
56 atctcaaacc cagcggcaac tcaccaagac attgacttcc tgattgaaga aatagaacgc 1740
57 cttggacaag atttataa                                                1758
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61 <211> LENGTH: 2382
62 <212> TYPE: DNA
63 <213> ORGANISM: Homo sapiens
65 <220> FEATURE:
66 <223> OTHER INFORMATION: 5' flanking region of gad2 gene nucleotides
68 <220> FEATURE:
69 <223> OTHER INFORMATION: R = G or A
71 <220> FEATURE:
72 <223> OTHER INFORMATION: Y = T or C
74 <220> FEATURE:
75 <223> OTHER INFORMATION: M = A or C
77 <220> FEATURE:
78 <223> OTHER INFORMATION: W = A or T
80 <220> FEATURE:
81 <223> OTHER INFORMATION: S = G or C
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85 gatttaaacg cttgctttta agaaccttta tgttttcaac cactcatcca tagtagaaaa 120
86 gttctgcaac cctagactgc tggcttgaag gaaaaccttt gcaggatttg atatggattt 180
87 caacaaagaa ccagcctctg cgaggctgga gagagctgcg gagctgccat gcctgaagtg 240
88 cagatggctg aaccacaagt ctttaggttt ccggagttgt tattgtggtg acctagagtg 300
89 tcagagccag gagagcaaga aagaggagcc aaactgagcc ctgagttttc gaccacccgg 360
90 gctcccacag cctggwacag acttcaccta gcacgctcag tgccagcctt cggcaggacg 420
91 ctatcaacgc ccgactggwt tcytgctctc atcctggcgc ctgggcccag ttgccatagt 480
92 gtggatccca tgactcctca gggaacccct ggactcaggc acgcgagaag aagacagcgc 540
93 tttgtggaga gaattgacca gggacagtta tgctcgagca cacaggactt gggcctgtat 600
94 gcgtccagca tgggccccag gatgtccctt ctaagcgagg gtcgaggggt gctcgcccag 660
95 acgggatccc cgggtctctg ctttgttagc agctttggtg gctggttcag gaggtcagag 720
96 aaataaaacg acttgtgaac acaatggaaa tgacaggcgc tctggccagg cgcggggaar 780
97 gcagccgcct cgggaagccg acctcagccc tttcctctct ctccctccct ccgtctcccc 840
98 cagagccccg gagctccgag gtgcacttga agttcatctc cactgccagg agaacgcagc 900
99 gcaaactgtc aaagggctcc caatccttag ggcgtcctcc ctgtctgcaa tagctttttg 960
100 tagaaaggaa atcatcagaa mgattctgac tttctcctcc tttctttatt agaaaaagag 1020
101 aaaccgcctc ctaatacgcc tcagagagaa ccaatctcgc gcttccgggt cacccgctac 1080
102 cgcgaagatt ctctgggggc gaggggggc attggtttga agcccttaa aacgagggcc 1140
103 ctgcaggcga tgccttcttt cctactcgga tttgtaaagc cgagattgct tagttggaaa 1200
104 ccctgttctc ccctcccagg cgcacacaga tccccttac acgcaagcag cgggcgcttc 1260
105 cacgcctccg cgggccaagg tcaccaaatg ccctgattcc atcccccacc cgccatcaat 1320
106 cctgccgact ctggccgctc tgcctcattc tcttccaaga agtttccatt cgtttattt 1380
107 tttttccccc agcccgaggt cctcagtaga ctccagcgtg gattttaatt gcctcaatca 1440
108 gcagtcattc tccccagccg tcactcagag cctggacggt gggtcccgcg atctagccct 1500
109 tggctacgca ggaacggtgc gcccccgggt acggcgcggt tcagcaggca ggcgtcaggt 1560
110 tctaccaagg cgctgaaatg agcccatcag cgggtaggag cccttccccc gccgtcccct 1620
111 ccccaggctc gtgaacggcg cctgatgccc gcccggggcg cgagctctcg aggtcgcagt 1680
112 gacctcagca cctgcttgga ggaaaacggc gcgggaaccc cgcttccttc ccctcagctg 1740
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113 gagccagacc tcaaacaaaa ccccaatcga tgcacacaga aaactcctct gggccacgct 1800
114 tcccgcctcg ccgaggtctc cccagtctgc ccctcgctga cgctggcgcg cagcsgctgt 1860
115 ggcagcaccc gggacagcgg ccgcccgcac ttcccgcctc tggctcgccc gaggacgcgc 1920
116 tggcacgcct cccaccccct cactctgact ccagctggcg tgcatggtct gcctcgcatc 1980
117 ctcacgactc agctccctcc ctctctcgtg tttttttcct ccgccgcccc ctcattcatc 2040
118 cccactgggc tccctttccc tcaaatgctc tggggctctc cgcgctttcc tgagtccggg 2100
119 ctccgaggac ccttaggtag tcccggtctc ttttaargct ccccggcttc caaagggttg 2160
120 ccacgtccct aaaccctgtc tccagctcgc atacacacac gcacagacac gcacgttttc 2220
121 tgttcctgcg tgacacccgc cctcgccgct cggccccgcc ggtccccgcg cggtgccctc 2280
122 ctcccgccac acgggcacgc acgcgcgcgc agggccaagc ccgaggcagc tcgcccgcag 2340
123 ctcgcactcg caggcgacct gctccagtct ccaaagccga tg                    2382
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 519
128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <220> FEATURE:
132 <223> OTHER INFORMATION: DNA-binding protein Ikaros (Lymphoid transcription factor
133       LyF-1)
135 <400> SEQUENCE: 3
136 Met Asp Ala Asp Glu Gly Gln Asp Met Ser Gln Val Ser Gly Lys Glu
137  1               5                  10                  15
139 Ser Pro Pro Val Ser Asp Thr Pro Asp Glu Gly Asp Glu Pro Met Pro
140              20                  25                  30
142 Ile Pro Glu Asp Leu Ser Thr Thr Ser Gly Gly Gln Gln Ser Ser Lys
143          35                  40                  45
145 Ser Asp Arg Val Val Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp
146      50                  55                  60
148 Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu
149 65                  70                  75                  80
151 Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His
152              85                  90                  95
154 Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu
155          100                 105                 110
157 Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Ile Cys Ile Gly
158          115                 120                 125
160 Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro
161      130                 135                 140
163 Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly Asn Leu
164 145                 150                 155                 160
166 Leu Arg His Ile Lys Leu His Ser Gly Glu Lys Pro Phe Lys Cys His
167              165                 170                 175
169 Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly His Leu
170              180                 185                 190
172 Arg Thr His Ser Val Gly Lys Pro His Lys Cys Gly Tyr Cys Gly Arg
173          195                 200                 205
175 Ser Tyr Lys Gln Arg Ser Ser Leu Glu Glu His Lys Glu Arg Cys His
176      210                 215                 220
178 Asn Tyr Leu Glu Ser Met Gly Leu Pro Gly Thr Leu Tyr Pro Val Ile
179 225                 230                 235                 240
```

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181 Lys Glu Glu Thr Asn His Ser Glu Met Ala Glu Asp Leu Cys Lys Ile
182             245             250             255
184 Gly Ser Glu Arg Ser Leu Val Leu Asp Arg Leu Ala Ser Asn Val Ala
185             260             265             270
187 Lys Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Gly Leu
188         275             280             285
190 Ser Asp Thr Pro Tyr Asp Ser Ser Ala Ser Tyr Glu Lys Glu Asn Glu
191     290             295             300
193 Met Met Lys Ser His Val Met Asp Gln Ala Ile Asn Asn Ala Ile Asn
194 305             310             315             320
196 Tyr Leu Gly Ala Glu Ser Leu Arg Pro Leu Val Gln Thr Pro Pro Gly
197             325             330             335
199 Gly Ser Glu Val Val Pro Val Ile Ser Pro Met Tyr Gln Leu His Lys
200             340             345             350
202 Pro Leu Ala Glu Gly Thr Pro Arg Ser Asn His Ser Ala Gln Asp Ser
203         355             360             365
205 Ala Val Glu Asn Leu Leu Leu Leu Ser Lys Ala Lys Leu Val Pro Ser
206     370             375             380
208 Glu Arg Glu Ala Ser Pro Ser Asn Ser Cys Gln Asp Ser Thr Asp Thr
209 385             390             395             400
211 Glu Ser Asn Asn Glu Glu Gln Arg Ser Gly Leu Ile Tyr Leu Thr Asn
212             405             410             415
214 His Ile Ala Pro His Ala Arg Asn Gly Leu Ser Leu Lys Glu Glu His
215         420             425             430
217 Arg Ala Tyr Asp Leu Leu Arg Ala Ala Ser Glu Asn Ser Gln Asp Ala
218         435             440             445
220 Leu Arg Val Val Ser Thr Ser Gly Glu Gln Met Lys Val Tyr Lys Cys
221     450             455             460
223 Glu His Cys Arg Val Leu Phe Leu Asp His Val Met Tyr Thr Ile His
224 465             470             475             480
226 Met Gly Cys His Gly Phe Arg Asp Pro Phe Glu Cys Asn Met Cys Gly
227             485             490             495
229 Tyr His Ser Gln Asp Arg Tyr Glu Phe Ser Ser His Ile Thr Arg Gly
230         500             505             510
232 Glu His Arg Phe His Met Ser
233         515
236 <210> SEQ ID NO: 4
237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
244 <400> SEQUENCE: 4
245 cctcaaatgc tctggggctc                                        20
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 20
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
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254 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
256 <400> SEQUENCE: 5
257 ggtgtcacgc aggaacagaa   20
260 <210> SEQ ID NO: 6
261 <211> LENGTH: 23
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
268 <400> SEQUENCE: 6
269 gtctctttta aagctccccg gct   23
272 <210> SEQ ID NO: 7
273 <211> LENGTH: 28
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 243
280 <400> SEQUENCE: 7
281 cgggctccga ggacccttag gtagtccc   28
285 <210> SEQ ID NO: 8
286 <211> LENGTH: 17
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb
293 <400> SEQUENCE: 8
294 ctgaggcgta ttaggag   17
297 <210> SEQ ID NO: 9
298 <211> LENGTH: 17
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb
305 <400> SEQUENCE: 9
306 ctcctaatac gcctcag   17
309 <210> SEQ ID NO: 10
310 <211> LENGTH: 16
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb
317 <400> SEQUENCE: 10
318 ggaaagcagc cgcctc   16
321 <210> SEQ ID NO: 11
322 <211> LENGTH: 30
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Chemically synthesized Primer to amplify SNP - 1.6 kb

VERIFICATION SUMMARY   DATE: 08/14/2006
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